

FIGURE 1

CBH1-E1 Fusion Construct

T. reesei cbh1 core, linker (no CBD)
+
Acidothermus cellulolyticus endoglucanase 1 core (E1)

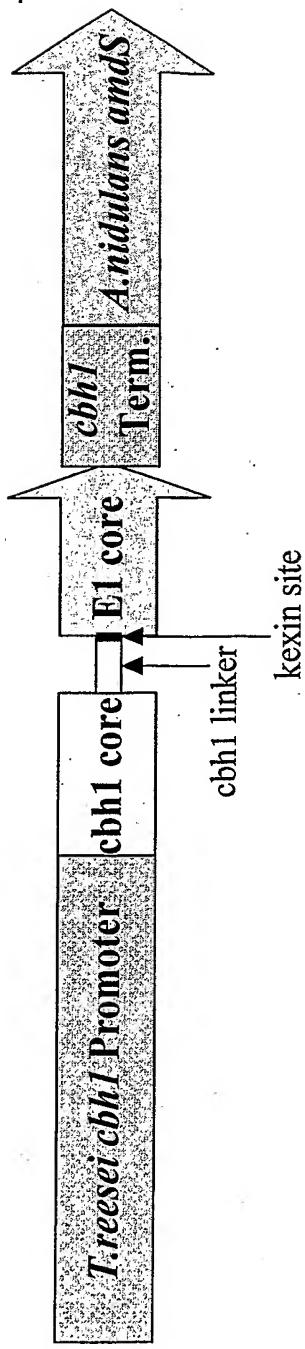


Figure 2

DNA sequence of *T.reesei cbh1* signal sequence+catalytic domain+linker (1570 bases)

ATGTATCGGAAGTTGGCCGTCATCTCGGCCTTCTGGCCACAGCTCGTGCTCA
GTCGGCCTGCACTCTCCAATCGGAGACTCACCCGCCTCTGACATGGCAG
AAATGCTCGTCTGGTGGCACTTGCACCAACAGACAGGGCTCCGTGGTCA
TCGACGCCAACTGGCGCTGGACTCACGCTACGAACAGCAGCACGAACGT
CTACGATGGCAACACTTGGAGCTCGACCCCTATGTCCTGACAACAGAGACC
TGCAGAAGAACTGCTGTGGACGGTGCCTACCGTCCACGTACG
GAGTTACCACGAGCGGTAACAGCCTCTCCATTGGCTTGTCACCCAGTC
TGCAGAAGAAACGTTGGCGCTCGCCTTACCTTATGGCGAGCGACACG
ACCTACCAGGAATTCACCCCTGCTTGGCAACGAGTTCTCTTCGATGTTGA
TGTTTCGCACTGCCGTAAGTGAATTACCATGAACCCCTGACGTATCTC
TTGTTGGCTCCCAGCTGACTGGCCAATTAAAGGTGCGGCTTGAACGGAG
CTCTCTACTTCGTTGCATGGACCGGGATGGTGGCGTGAGCAAGTATCC
CACCAACACCGCTGGGCCAAGTACGGCACGGGTACTGTGACAGCCAG
TGTCCCCGCGATCTGAAGTTCATCAATGGCCAGGCCAACGTTGAGGGCT
GGGAGCCGTATCCAACAAACGCAAACACGGGATTGGAGGACACGGAA
GCTGCTGCTCTGAGATGGATATCTGGGAGGCCAACCTCCATCTCGAGGC
TCTTACCCCCCACCCTTGACGACTGTCGGCCAGGAGATCTGCAGGGT
GATGGGTGCGGCCGAACTTACTCGATAACAGATATGGCGGCACTTGC
ATCCCGATGGCTGCGACTGGAACCCATACCGCCTGGCAACACCCAGCTT
CTACGGCCCTGGCTCAAGCTTACCCCTGACGACCAAGAAATTGACC
GTTGTCACTTCAAGCTGAGACGTCGGGTGCCATCAACCGATACTATGTCC
AGAATGGCGTCACTTCCAGCAGCCAACGCCAGCTGGTAGTTACTC
TGGCAACGAGCTAACGATGATTACTGCACAGCTGAGGAGGCAGAATT
GGCGGATCCTCTTCTCAGACAAGGGCGGCTGACTCAGTTCAAGAAGG
CTACCTCTGGCGGCATGGTCTGGTCATGAGTCTGTGGATGATGTGAG
TTTGATGGACAAACATGCGCGTTGACAAAGAGTCAAGCAGCTGACTGAG
ATGTTACAGTACTACGCCAACATGCTGTGGCTGGACTCCACCTACCCGA
CAAACGAGACCTCCTCCACACCCGGTGCCGTGCGCGGAAGCTGCTCCAC
CAGCTCCGGTGTCCCTGCTCAGGTGCAATCTCAGTCTCCAAACGCCAAG
GTCACCTCTCCAACATCAAGTTCGGACCCATTGGCAGCACCACCGAAC
CTAGCGGCCGGCAACCCCTCCGGGAAACCCGCCCTGGCACCCACCCACCG
CCGCCAGCCACTACCACTGGAAGCTCTCCGGACCTACTAGT

Figure 3

Amino acid sequence of *T.reesei cbh1* signal sequence + catalytic domain + linker (480 amino acids)

MYRKLAVISAFLATARAQSACTLQSETHPPLTWQKCSSGGTCTQQTGSVVID
ANWRWTHATNSSTNCYDGNTWSSTLCPDNETCAKNCCLDGAAYASTYGVT
TSGNSLSIGFVTQSAQKNVGARLYLMASDTTYQEFTLLGNEFSFDVDVSQLP
CGLNGALYFVSMADGGVSKYPTNTAGAKYGTGYCDSQCPRDLKFINGQA
NVEGWEPSSNNANTGIGGHGSCCSEMDIWEANSISEALTPHPCTTVGQEICE
GDGCGGTYSDNRYGGTCDPDGCDWNPYRLGNTSFYGPSSFTLDDTTKKLT
VVTQFETSGAINRYVQNGVTFQQPNAELGSYSGNELNDYCTAEEAEFGG
SSFSDKGLTQFKATSGGMVLVMSLWDDYYANMLWLDSTYPTNETSSTP
GAVRGSCSTSSGVPAQVESQSPNAKVTFSNIKFGPIGSTGNPSGGNPPGGNPPG
TTTTRRPATTTGSSPGPTS

Figure 4

DNA sequence of *Acidothermus cellulolyticus* GH5A endoglucanase 1 catalytic domain (1077 bases)

GCAGGGCGGCGGCTATTGGCACACGAGCGGCCGGGAGATCCTGGACGCGAAC
AACGTGCCGGTACGGATGCCGGCATCAACTGGTTGGGTTCGAAACCTGCA
ATTACGTCGTGCACGGTCTCTGGTCACGCAGTACCGCAGCATGCTCGACCA
GATAAAAGTCGCTCGGCTACAACACAATCCGGCTGCCGTACTCTGACGACATT
CTCAAGCCGGGCACCATGCCAACAGCATCAATTTCACCAAGATGAATCAGG
ACCTGCAGGGTCTGACGTCTTGACGGTCACTGGACAAAATCGTCGCGTACGC
CGGTCAAGATCGGCCTGCGCATCATTCTGACCGCCACCGACCGGATTGCAGC
GGGCAGTCGGCGCTGTGGTACACGAGCAGCGTCTCGGAGGGTACGTGGATT
CCGACCTGCAAGCGCTGGCGCAGCGCTACAAGGGAAACCGACGGTCTCG
GCTTGACTTGACAACGAGCCGCATGACCCGGCTGCTGGGCTGCGCGA
TCCGAGCATCGACTGGCGATTGGCCGAGCGGGCGAAACGCCGTGCTC
TCGGTGAATCCGAAACCTGCTCATTTCGTCGAAGGTGTGCAGAGCTACAACG
GAGACTCCTACTGGTGGGGCGAACCTGCAAGGAGGCCGCCAGTACCCGGT
CGTGTGAACGTGCCAACGCCCTGGTGTACTCGCGCAGCACTACGCGACG
AGCGTCTACCCGACAGCTGGTTCAAGCGATCCGACCTTCCCCAACACATGC
CCGGCATCTGGAACAAGAACTGGGGATACCTCTTCATCAGAACATTGCACC
GGTATGGCTGGCGAATTGGTACGACACTGCAATCCACGACCGACCAGACG
TGGCTGAAGACGCTCGTCCAGTACCTACGGCCGACCGCGCAATACGGTGC
ACAGCTTCAAGGATGACTGGCAGACGGTCGACACAGTAAAAGACGGCTAT
CTCGCGCCGATCAAGTCGTGATTTCGATCCTGTCGGC

Figure 5

Amino acid sequence of *Acidothermus cellulolyticus* GH5A endoglucanase 1 catalytic domain (359 amino acids)

AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNYVVHGLWSRDYRSMLDQIKSLGYNTIRLPYSDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIGLRIILDRHRPDCSGQSAWLWYTSSVSEATWISDLQALAQRYKGNPTVVGFDLHNEPHDPACWGCGDPSIDWRLAAERAGNAVLSVNPNLLIFVEGVQSYNGDSYWWGGNLQGAGQYPVVLNVPNRLVYSAHDYATSVYPQTWFSDPTFPNNMPGIWNKNWGYLFNQNIAPVWLGEFGTTLQSTTDQTLKTLVQYLRPTAQYGADSFQWTFWSWNPDSGDTGGILKDDWQTVDTVKDGYLAPIKSSIFDPVG

FIGURE 6

DNA sequence of *Acidothermus cellulolyticus* GH48 cellulase catalytic domain (1914 bases)

AACGACCCGTACATCCAGCGGTTCTCACGATGTACAACAAGATTACGACC
CAGCGAACGGCTACTTCAGCCGCAGGGATTCCCTACCACTCGGTAGAAAC
GCTCATCGTGAGGCACCAGACTACGGGCACGAGACAACCTCGGAGGCCTAC
AGCTTCTGGCTCTGGCTCGAACGCGACGTACGGCGCAGTGACCGGCAACTGGA
CGCCGTTCAACAACGCCTGGACGACGTACGGGAAACGTACATGATCCCAGCA
CGCGGACCAGCCAACAACCGCGTCAACACCCAACAGGCCGGCGTAC
GCTCCGGAAGAGCCGCTGCCAGCATGTACCCGGTTGCCATCGACAGCAGCG
TGCCGGTTGGGCACGACCCGCTGCCGCCAATTGCACTCGACGTACGGCAC
TCCGGACATTACGGCATGCACTGGCTGGCGACGTTGACAACATCTACGGA
TACGGCGACAGCCCCGGCGGTGGTTGCGAACACTGGCTCTCCGCTAACGGCG
TCTCCTACATCAACACATTCCAGCGCGCTCGCAGGAGTCCGCTGGGAGAC
GGTCACCCAGCCGACGTGCGAACACGGCAAGTACGGTGGGGCGCACGGCTA
CGTCGACCTGTTCATCCAGGGTTGACGCCCGCAGTGGAAAGTACACCGAT
GCCCGGACGCCGACGCCGTGCCGTCCAGGCTCGTACTGGCCTACACCT
GGGCATCGCGCAGGGCAAGGCAAGCGCGATTGCCCGACGATGCCAAGG
CGGCCAAACtCGGCGACTACCTGCGGTACTCGCTTTGACAAGTACTTCAAG
CAGGTCGGCAACTGCTACCCGGCAGCTCCTGCCCTGGAGCAACCGGACGCC
AGAGCGAGACCTACCTGATCGGCTGGTACTACGCCCTGGGGCGCTCAAGCCA
AGGCTGGGCTGGCGATTGGTGACGGCGCCGACTTCGGCTACCGAAT
CCGCTTGGCGTGGCGATGTCGAACGTGACACCGCTATTCCGCTTCGCC
CACGGCAAAGAGCGACTGGCGGAGCTTGCAAGCGCCAGCTGGAGTTCTAC
CAGTGGTTGCAATCCGCGGAAGGAGCCATTGCGGGCGGCCACCAACAGCT
GGAACGGCAATTACGGGACCCCGCCGGAGACTCGACCTTACGGCAT
GGCGTACGACTGGAGCCGGTCTACACGACCCGCCAGCAACAACGGTTC
GGCTCCAGGCCTGGTCCATTGGAACGGGTTGCCGAGTACTACTACGTCACCG
GCGACCCGAAGGCCAAGGCCTGCTCGACAAGTGGGTCGATGGGTGAAGC
CGAATGTCACCACCGGTGCTCATGGTCGATTCCGTCGAATTGCTCTGGAGC
GGCCAACCGGATACTGGGAATCCGAGCAACCCAGGAACGAATGCCAACCTG
CACGTGACCATCACGTCGTCGGCGAGGACGTCGGTGTGCCGGCGCTCG
CGAAGACACTCGAGTACTACGCCGAAATCCGGCGATAACGCCCTCGCGCA
CCTCGCGAAGGGATTGCTGACTCCATGTGGAACAAACGACCAGGACAGCCTC
GGTGTGAGCACACCGGAGACGCCGGACCGACTACTCTCGGTTCACTCAGGTGT
ACGACCCGACGACTGGTGACGGCCTCTACATCCCGTGGGTTGGACGGGGAC
CATGCCAACGGTACCAAGGATCCGAGTGGTCGAAGGTGCAGGCCTACCTCAACG
TCCTGGTACACCAAGGATCCGAGTGGTCGAAGGTGCAGGCCTACCTCAACG
GCGGGCCTGCTCCGACGTTCAACTACCACCGGTTCTGGGGAGTCCGACTT
CGCGATGGCGAACGCCGATTGGCATGCTCTCCATCCGGG

FIGURE 7

Amino acid sequence of *Acidothermus cellulolyticus* 48 catalytic domain (638 amino acids)

NDPYIQRFLTMYNKIHD PANGYFSPQGIPYHSVETLIVEAPDYGHETTSEAYSFW
LWLEATYGA VTGNWTPFNNAWTTMETYMPQHADQPNNASYNPNSPAS YAPEE
PLPSMYPVAIDSSVPVGHDPLAAELQSTYGT PDIYGMHWLADV DNIYGYGDSPG
GGCELGPSAKGVSYINTFQRGSQESVWETVTQPTCDNGKYGGAHGYVDLFIQGS
TPPQWKYTDAPDADARAVQAAYW AYT WASA QGKASAIAPTI AKA AKLGDYLR
YSLFDKYFKQVGNCYPASSCPGATGRQSETYLIGWYYAWGGSSQGWAWRIGD
GAAHFGYQNPLAAWAMSNTPLIPLSPTAKSDWAASLQRQLEFYQWLQSAEGA
IAGGATNSWNGNYGTPPAGDSTFYGMAYDWE PVYHDPPSNNWFGFQAWSMER
VAEYYYVTGDPKAKALLDKWVAWVKPNVTGASWSIPSNLWSGQPDTWNPS
NPGTNANLHVTITSSGQDVGVAAALAKTLEYYAAKSGDTASRDLAKGLLDSMW
NNDQDSLGVSTPETR TDYSRFTQVYDPTTGDGLYIPSGWTGTMPNGDQIKPGAT
FLSIRSWYTKDPQWSKVQAYLNGGPAPTFNYHRFWAESDFAMANADFGMLFPS
G

FIGURE 8A

DNA sequence of *Acidothermus cellulolyticus* GH74 catalytic domain

GCGACGACTCAGCCGTACACCTGGAGCAACGTGGCGATCGGGGGCGGCGGC
TTTGTGACGGGATCGTCTTCAATGAAGGTGCACCGGAATTCTGTACGTGCG
GACGGACATCGGGGGATGTATCGATGGGATGCCGCCAACGGCGGTGGAT
CCCTCTTCTGGATTGGGTGGATGGAACAATTGGGGTACAACGGCGTCGTC
AGCATTGCGGCAGACCCGATCAATACTAACAAAGGTATGGGCCGCGTCGGAA
TGTACACCAACAGCTGGACCCAAACGACGGAGCGATTCTCCGCTCGTCTGA
TCAGGGCGCAACGTGGCAAATAACGCCCTGCCGTTCAAGCTTGGCGGCAAC
ATGCCCGGGCGTGGATGGCGAGCGGCTTGCCTGGATCCAAACAATGACA
ACATTCTGTATTCCGGCGCCCCGAGCGGCAAAGGGCTCTGGAGAAGCACAGA
TTCCGGCGCGACCTGGTCCCAGATGACGAACCTTCCGGACGTAGGCACGTAC
ATTGCAAATCCCAGTGACACGACCGGCTATCAGAGCGATATTCAAGGCGTCG
TCTGGGTGCGTTCGACAAGTCTCGTCATCGCTGGCAAGCGAGTAAGACC
ATTTTGTTGGCGTGGCGGATCCCAAATAATCCGGTCTTCTGGAGCAGAGACG
GCGCGCGACGTGGCAGCGGTGCCGGTGCCTGCCGACCGGCTTCATCCGCA
CAAGGGCGTCTTGACCCGGTCAACCACGTGCTCTATTGCCACCAGCAAT
ACGGGTGGTCCGTATGACGGGAGCTCCGGGACGTCTGGAAATTCTCGGTGA
CCTCCGGACATGGACCGAATCAGCCGGTACCTCGACGGACACGGCAA
CGACTACTTGGTTACAGCGGCTCACTATCGACCGCCAGCACCGAACACG
ATAATGGTGGCAACCCAGATATCGTGGTGGCCGGACACCATAATCTTCGGA
GCACCGACGGCGGTGCGACGTGGACCGGGATCTGGATTGGACGAGTTATCC
CAATCGAAGCTTGCATATGTGCTTGACATTCCGGAGCCTTGGCTGACCT
TCGGCGTACAGCCGAATCCTCCGTACCGAGTCCGAAGCTCGGCTGGATGGA
TGAAGCGATGGCAATCGATCCGTTCAACTCTGATCGGATGCTCTACGGAACA
GGCGCGACGTTGTACGCAACAAATGATCTCACGAAGTGGACTCCGGCGGCC
AGATTCATATCGCGCCGATGGTCAAAGGATTGGAGGAGACGGCGGTAAACG
ATCTCATCAGCCCAGCGTCTGGCGCCCGCTCATCAGCGCTCTCGGAGACCTC
GGCGGCTTCACCCACGCCGACGTTACTGCCGTGCCATCGACGATCTCACGTC

FIGURE 8B

ACCGGTGTTCACGACCGGCACCAGCGTCGACTATGCGGAATTGAATCCGTCG
ATCATCGTCGCGCTGGAAGTTCGATCCATCGAGCCAACCGAACGACAGGC
ACGTCGCGTTCTCGACAGACGGCGGCAAGAACTGGTTCCAAGGCAGCGAAC
TGGCGGGGTGACGACGGCGGCACCGTCGCCGCATGGCCGACGGCTCTCGT
TTCGTCTGGCTCCCGCGATCCCGTCAGCCTGTGGTACGCAGTCGGATT
TGGCAACTCCTGGCTGCTCGCAAGGTGTTCCGCCAATGCCAGATCCGCT
CAGACCGGGTGAATCCAAAGACTTCTATGCCCTATCCAATGGAACCTTCTAT
CGAACGACGGACGGCGGTGACATTCCAACCGTCGCCGCCGGTCTCCGA
GCAGCGGTGCCGTCGGTGTATGTTCCACGCGGTGCCTGGAAAAGAACGGGA
TCTGTGGCTCGCTGCATCGAGCGGGCTTACCACTCAACCAATGGCGGCAGC
AGTTGGTCTGCAATCACCGCGTATCCTCCGCGGTGAACGTGGGATTGGTA
AGTCTGCGCCCGGGCGTACCGCTCCGACGACGGTGGACGACCTGGGTACGG
GGCGTTACGGGGCGTACCGCTCCGACGACGGTGGACGACCTGGGTACGG
ATCAATGATGACCAGCACCAATACGGAAATTGGGGACAAGCAATCACCGGTG
ACCCCGGAATTACGGCGGGTGTACATAGGCACGAACGGCCGTGGAATTGT
CTACGGGGACATTGGTGGTGCGCCGTCCGGATCG

FIGURE 9

Amino acid sequence of *Acidothermus cellulolyticus* 74 catalytic domain (741 amino acids)

ATTQPYTWSNVAIGGGFVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPL
LDWVGWNNWGYNGVVSIAADPINTNKVWAAGVGMYTNSWDPNDGAILRSSDQ
GATWQITPLPFKLGGNMPGRGMGERLAVDPNNNDNILYFGAPSGKGLWRSTDG
ATWSQMTNFDPDVGTYIANPTDTGYQSDIQGVVVWAFDKSSSLGQASKTIFVG
VADPNNPVFWSRDGGATWQAVPGAPTGFIPHKGVFDPVNHVLYIATSNTGGPY
DGSSGDVWKFSVTSGTWTRISPVPSTDANDYFGYSLTIDRQHPNTIMVATQIS
WWPDTIIFRSTDGGATWTRIWDWTSYPNRSLRYVLDISAEPWLTGVQPNPPVPS
PKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTWKWDGGQIHIAPMVKGLE
ETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSDYAEELNP
SIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGVTTGGTVAASADGSRFV
WAPGDPGQPVYYAVFGNSWAASQGVPANAQIRSDRVNPKTFYALSNGTFYRS
TDGGVTFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWS
AITGVSSAVNVFGFKSAPGSSYPAVFVVGVTIGGVTGAYRSDDGGTTWVRINDDQ
HQYGNWGQAITGDPRIYGRVYIGTNGRGIVYGDIGGAPSGS

Figure 10

DNA sequence of *Thermobifida fusca* E3 (TfE3) cellulase including the cellulose binding domain - linker - catalytic domain but lacking a TfE3 signal sequence. (1677 bases)

GCCGGCTGCTCGGTGGACTACACGGTCAACTCCTGGGGTACCGGGTTACCG
CCAACGTCAACCATACCAACCTCGGCAGTGCATCAACGGCTGGACCCCTGG
GTGGGACTTCCCCGGCAACCAGCAGGTGACCAACCTGTGGAACGGGACCTAC
ACCCAGTCGGGCAGCACGTGTCGGTCAGCAACGCCCGTACAACGCCCTCCA
TCCCGGCCAACGGAACGGTGAGTTGAGTCGGGTTAACGGCTCCTACTCGGGCAG
CAACGACATCCCCCTCCTCAAGCTGAACGGGTTACCTGCGACGGCTCG
GACGACCCCGACCCCGAGCCCAGCCCCCTCCCCCAGCCCTCCCCCAGCCCCA
CAGACCCGGATGAGCCGGCGGCCGACCAACCCGCCACCAACCCCGCG
AGAAGGTGACAAACCGTTCGAGGGCGCCAAGCTGTACGTGAACCCGGTCTG
GTCGGCCAAGGCCGCCGCTGAGCCGGCGGTTCCCGCGGTGCGCAACGAGTCC
ACCGCTGTCTGGCTGGACCGTATCGCGCCATCGAGGGCAACGACAGCCGA
CCACCGGCTCCATGGGTCTGCGCACCACCTGGAGGGAGGCCGTCCGCCAGTC
CGGTGGCGACCCGCTGACCATCCAGGTGTCATCTACAAACCTGCCGGCCGC
GACTGCGCCCGCTGGCCTCAACGGTGAGCTGGTCCCGATGAACTCGACC
GCTACAAGAGCGAGTACATCGACCCGATCGCCGACATCATGTGGGACTTCGC
AGACTACGAGAACCTGCGGATCGTCGCCATCATCGAGATCGACTCCCTGCC
AACCTCGTACCAACGTGGCGGGAACGGCGGCCACCGAGCTCTGCGCCTACA
TGAAGCAGAACGGCGGCTACGTCAACGGTGCGCTACGCCCTCGCAAGCT
GGCGAGATCCCGAACGTTACAACATCGACGCCGCCACACGGCTGG
ATCGGCTGGACTCCAACCTCGGCCCTCGGTGGACATCTTCTACGAGGCCG
CCAACGCCCTCCGGCTCCACCGTGGACTACGTGACGGCTCATCTCCAACAC
GGCCAACTACTCGCCACTGTGGAGGCCGTACCTGGACGTCAACGGCACCGTT
AACGGCCAGCTATCCGCCAGTCCAAGTGGGTTGACTGGAACCAAGTACGTG
ACGAGCTCTCCTCGTCCAGGACCTGCGTCAGGCCCTGATCGCCAAGGGCTTC
CGGTCCGACATCGGTATGCTCATCGACACCTCCCGCAACGGCTGGGTGGCC
CGAACCGTCCGACCGGACCGAGCTCCACCGACCTCAACACCTACGTG
CGAGAGCCGTATCGACCGCCGTATCCACCCCGTAACGGTCAACCCGGCTCCGGTGTGACG
GGTGGGGCCTCGCGAGCGGCCACGGTCAACCCGGCTCCGGTGTGACG
CCTACGTCTGGGTGAAGCCCCGGGTGAGTCCGACGGGCCAGCGAGGAGAT
CCCGAACGACGAGGGCAAGGGCTTCGACCGCATGTGCGACCCGACCTACCAG
GGCAACGCCCGAACGGCAACAAACCCCTCGGTGCGCTGCCAACGCC
TCTCCGGCCACTGGTTCTGCCCAGTTCCCGAGCTGCTGGCCAACGCC
CCGCCTCTGTAA

Figure 11

Amino acid sequence of the *Thermobifida fusca* E3 - cellulase including the cellulose binding domain - linker – catalytic domain but lacking the TfE3 signal sequence. (558 amino acids)

AGCSVDTVNSWGTGFTANVTITNLGSAINGWTLEWDFPGNQQVTNLWNGTYT
QSGQHVSVSNAAPYNSIPANGTVEFGFNGSYGSNDIPSSFKLNGVTCDGSDDPD
PEPSPSPSPSPSPTDPDEPGGPTNPPTNPGEKVDNPFEAGAKLYVNPVWSAKAAAEP
GGSAVANESTAVWLDRIGAIEGNDSPTTGSMGLRDHLEEAVRQSGGDPLTIQVVI
YNLPGRDCAALASNGLGPDELDRYKSEYIDPIADIMWDFADYENLRIVAIIEIDS
LPNLVTNVGGNGGTTELCA YMKQNNGGYVNGVGYALRKLGEIPNVYNYIDAHH
GWIGWDSNFGPSVDIFYEAANASGSTVDYVHGFISNTANYSATVEPYLDVNGTV
NGQLIRQSKWVDWNQYVDELSFVQDLRQALIAKGFRSDIGMLIDTSRNGWGGP
NRPTGPSSTDLN TYVDESRIDRRIHPGNWCNQAGAGLGERPTVNPAPGVDAYV
WVKPPGESDGASEEIPNDEGKGFDRCMCDPTYQGNARNGNNPSGALPNAPISGH
WFSAQFRELLANAYPPL

Figure 12

DNA sequence of *Thermobifida fusca* E5 (TfE5) endoglucanase including the cellulose binding domain - linker and catalytic domain but lacking a TfE5 signal sequence. (1293 bases)

GGCGGTCTCACGCCACAGTCACCAAAGAACCTCGTGGGACAACGGCTACT
CCCGGTCCGTCACCGTCCGCAACGACACCTCGAGCACCCTCAGTGGGA
GGTCGTCTCACCCGCCGGCGGACTACAGTGGCCAGGTGTGGAACGCC
CAGCACACCAGCAGCGGCAACTCCCACACCTTACCCGGGTTCTGGAACA
GCACCATCCCGCCGGAGGCACCGCCTCTCCGGCTCATCGCTCCGGCAGC
GGCGAACCCACCCACTGCACCATCAACGGGCCCTCGCACGAAGGCTCG
AGCCGGCGGCCCGGCGGTCCCGGAACCCCTCCCCGACCCGGCACGCA
GCCCGGCACCGGCACCCCGGTGAGCGGTACGGCAAAGTCCAGGTCTGCC
ACCCAGCTCTGCGACGAGCACGGCAACCCGGTCAAACGCGCGGATGAGCA
CCACGGCATCCAGTGGTTCGACCACTGCCTGACCGACAGCTCGCTGGACGC
CCTGGCCTACGACTGGAAGGCCGACATCATCCGCTGTCCATGTACATCCAG
GAAGACGGTACGAGACCAACCCGCGCGCTCAACGACGGATGCACCAG
CTCATCGACATGGCCACGGCGCGCGCTGTACGTGATCGTGGACTGGCACA
TCCTCACCCGGCGATCCCCACTACAACCTGGACCGGGCCAAGACCTTCTC
GCGGAAATCGCCCAGGCCACGCCAGCAAGACCAACGTGCTTACGAGATCG
CCAACGAACCCAACGGAGTGAGCTGGGCCTCCATCAAGAGCTACGCCGAAG
AGGTCACTCCGGTGTACGCCAGCGCAGCCGACTCGGTGATCATCGTGGG
CACCCGCGCTGGTCGCTCGCGTCTCGAAGGCTCCGGCCCGCCGAG
ATCGCGGCCAACCCGGTCAACGCCCTCAAACATCATGTACGCCCTCAACTCTA
CGCGGCCCTCGCACCGCACAACACCTCAACCGCGTGCCTGAGGCCTCCGAG
CTGTTCCCGGTCTCGTCACCGAGTTGGCACCAGACCTACACCGGTGACG
GCGCCAACGACTTCCAGATGGCCGACCGCTACATCGACCTGATGGCGGAACG
GAAGATCGGGTGGACCAAGTGGAAACTACTCGGACGACTTCCGTTCCGGCG
GTCTCCAGCCGGGACCTGCGCTCCGGCCCGTGGAGCGGTTCGTCGC
TGAAGGCGTCCGGACAGTGGGTGCGGAGCAAGCTCCAGTCCTGA

Figure 13

Amino acid sequence of the *Thermobifida fusca* E5 -cellulase including the cellulose binding domain - linker - catalytic domain but lacking a TfE5 signal sequence. (430 amino acids)

AGLTATVTKESSWDNGYSASVTVRNDTSSTVSQWEVVLTPGGTTAQVWNAQ
HTSSGNSHTFTGVWNSTIPPGTASSGFIASGSGEPTHCTINGAPCDEGSEPGGP
GGPGTPSPDPGTQPGTGTVERYGKVQVCGTQLCDEHGNPQLRGMSTHGIQW
FDHCLTDSSLDALAYDWKADIIRLSMYIQEDGYETNPRGFTDRMHQLIDMATAR
GLYVIVDWHILTPGDPHYNLDRAKTFFAEIAQRHASKTNLYEIANEPNGVSWA
SIKSYAEEVIPVIRQRDPDSVIIVGTRGWSSLGVSEGSGPAEIAANPVNASNIMYAF
HFYAASHRDNYLNALREASELFPVFVTEFGTETYTGDGANDFQMADRYIDLMA
ERKIGWTKWNYSDDFRSGAVFQPGTCASGGPWGSSLKASGQWVRSKLQS

Figure 14

DNA sequence of CBH1-E1 fusion (2656 bases)

T.reesei cbh1 signal sequence+catalytic domain+linker+added amino acids
 SKR+*Acidothermus cellulolyticus* GH5A catalytic domain

ATGTATCGGAAGTTGGCCGTATCTGGCCTTCTGGCACAGCTCGTGCTCA
 GTCGGCCTGCACTCTCAATCGGAGACTCACCCGCCCTGACATGGCAGAAA
 TGCTCGTCTGGTGGCACTTGCACTCACAGACAGCAGCTCCGTGGTCATCGACG
 CCAACTGGCGCTGGACTCACGCTACGAACAGCAGCACGAACCTGCTACGATGG
 CAACACTTGGAGCTGACCCCTATGCTCTGACAACAGAGACCTGCGCGAAGAAC
 TGCTGTCTGGACGGTGCCCTACCGTCCACGTACGGAGTTACCAACGAGCG
 GTAACAGCCTCTCCATTGGCTTGTCAACCCAGTCTGCGCAGAAGAACGTTGGC
 GCTGCCCTTACCTTATGGCGAGCGACACGACCTACCAAGGAATTCACCTGCT
 TGGCAACGAGTTCTTCTCGATGTTGATGTTCGCAGCTGCCGTAAGTGA
 ACCATGAACCCCTGACGTATCTTCTGTGGGCTCCAGCTGACTGGCCA
 AAGGTGCGGCTTGAACGGAGCTCTACTCGTGTCCATGGACGCGGATGGT
 GGCCTGAGCAAGTATCCCACCAACACCGCTGGCGCCAAGTACGGCACGGGGT
 ACTGTGACAGCCAGTGTCCCCCGCATCTGAAGTTCATCAATGGCCAGGCCAA
 CGTTGAGGGCTGGGAGCCGTATCCAACAAACGCAAACACGGGCATTGGAGG
 ACACCGGAAGCTGCTCTGAGATGGATATCTGGGAGGCCACTCCATCTCC
 GAGGCTCTACCCCCCACCCTGACGACTGTGGCCAGGAGATCTGCGAGG
 GTGATGGGTGCGGCGGAACCTACTCCGATAACAGATATGGCGGCACTTGC
 TCCCGATGGCTGCGACTGGAACCCATACCGCTGGCAACACCAGCTTAC
 GGCCCTGGCTCAAGCTTACCTCGATACCAAGAAATTGACCGTTGTAC
 CCAGTTGAGACGTCGGGTGCCATCAACCGATACTATGTC
 CAGCTCAACGCTCAAGCAGCTGAGCTGGTAGTTACTCTGGCAACGAGCTCA
 ACGATGATTACTGCACAGCTGAGGAGGCAGAATTGGCGGATCCTCTTCTC
 AGACAAGGGCGGCCCTGACTCAGTTCAAGAAAGGCTACCTCTGGCGGATGGT
 CTGGTCATGAGTCTGTGGGATGATGTGAGTTGATGGACAAACATGCGCGTT
 GACAAAGAGTCAGCAGCTGACTGAGATGTTACAGTACTACGCCAACATGCT
 GTGGCTGGACTCCACCTACCGACAAACGAGACCTCCTCACACCCGGTGC
 GTGCGCGGAAGCTGCTCCACCAGCTCCGGTGTCCCTGCTCAGGTGCAATCTC
 AGTCTCCCAACGCCAACGGTCACCTTCTCCAACATCAAGTTCGGACCCATTGGC
 AGCACCGGCAACCCCTAGCGGCGGCAACCCCTCCCGCGGAAACCCGCTGGCA
 CCACCAACCACCCGCCGCCAGCCACTACCAACTGGAAAGCTCTCCGGACCTAC
 TAGTAAGCGGGCGGGCGGGCTATTGGCACACGAGCGGCCGGAGATCCT
 GGACGCGAACAAACGTGCCGGTACGGATGCCGGCATCAACTGGTTGGGTT
 GAAACCTGCAATTACGTCGTGCACGGTCTCTGGTCACGCGACTACCGCAGCA
 TGCTCGACCAGATAAAGTCGCTCGGCTACAACACAATCCGGCTGCCGTACTC
 TGACGACATTCTCAAGCCGGGACCATGCCAACAGCATCAATTTC
 ATGAATCAGGACCTGCAGGGTCTGACGTCTTGCAAGGT
 TCGCGTACGCCGGTCAGATCGGCCTGCGCATCTTGA
 GGATTGCAGCGGGCAGTCGGCGCTGTGGTACACGAGCAGCGTCTCGGAGGGT
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GCCGTGCTCTCGGTGAATCCGAAACCTGCTCATTTCGTCGAAGGTGTGCAGAG
CTACAACGGAGACTCCTACTGGTGGGGCGGCAACCTGCAAGGAGCCGGCCA
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ACAACATGCCCGGCATCTGGAACAAGAACGACTGGGGATACCTCTCAATCAGAA
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GACCAGACGTGGCTGAAGACGCTCGTCCAGTACCTACGGCCGACCGCGCAAT
ACGGTGC GGACAGCTCCAGTGGACCTTCTGGTCTGGAACCCCCGATTCCGG
CGACACAGGAGGAATTCTCAAGGATGACTGGCAGACGGTCGACACAGTAAA
AGACGGCTATCTCGCGCCGATCAAGTCGTGATTTCGATCCTGTCGGCTAA

Figure 15

Amino acid sequence of CBH1-E1 fusion (841 amino acids)

T.reesei cbh1 signal sequence+catalytic domain+linker+added amino acids
SKR+*Acidothermus cellulolyticus* GH5A catalytic domain

MYRKLAVisAFLATARAQSACTLQSETHPPLTWQKCSSGGTCTQQTGSVVIDAN
WRWTHATNSSTNCYDGNTWSSTLCPDNETCAKNCCLDGAAYASTYGVTTSGNS
LSIGFVTQSAQKNVGarLYLMASDTTYQEFTLLGNEFSFDVDSLPCGLNGAL
YFVSMADGGVSKYPTNTAGAKYGTGYCDSQCPRDLKFINGQANVEGWEPSSN
NANTGIGGHGSCCSEMDIWEANSISEALTPHPCTTVGQEICEGDGCGGTYSNDRY
GGTCDPDGCDWNPYRLGNTSFYGPGSSFTLDTKKLTVVTQFETSGAINRYYVQ
NGVTFQQPNAELGSYSGNELNDDYCTAEEAEFGGSSFSDKGGLTQFKKATSGGM
VLVMSLWDDYYANMLWLDSTYPTNETSSTPGAVRGSCSTSSGVPAQVESQSPN
AKVTFSNIKFGPIGSTGNPSGGNPPGGNPPGTTTRRPATTGSSPGPTSKRAGGG
YWHTSGREILDANNVPVRIAGINWFGFETCNYVVHGLWSRDYRSMILDQIKSLGY
NTIRLPYSDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIGLRILD
RHRPDCSGQSAWYTSSVSEATWISDLQALAQRYGNPTVVGFDLHNEPHDPAC
WGCGDPSIDWRLAAERAGNAVLSVNPNLLIFVEGVQSYNGDSYWWGGNLQGA
GQYPVVLNVPNRLVYSAHDYATSVYPQTWFSDFPTFPNNMPGIWNKNWGYLFN
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Figure 16

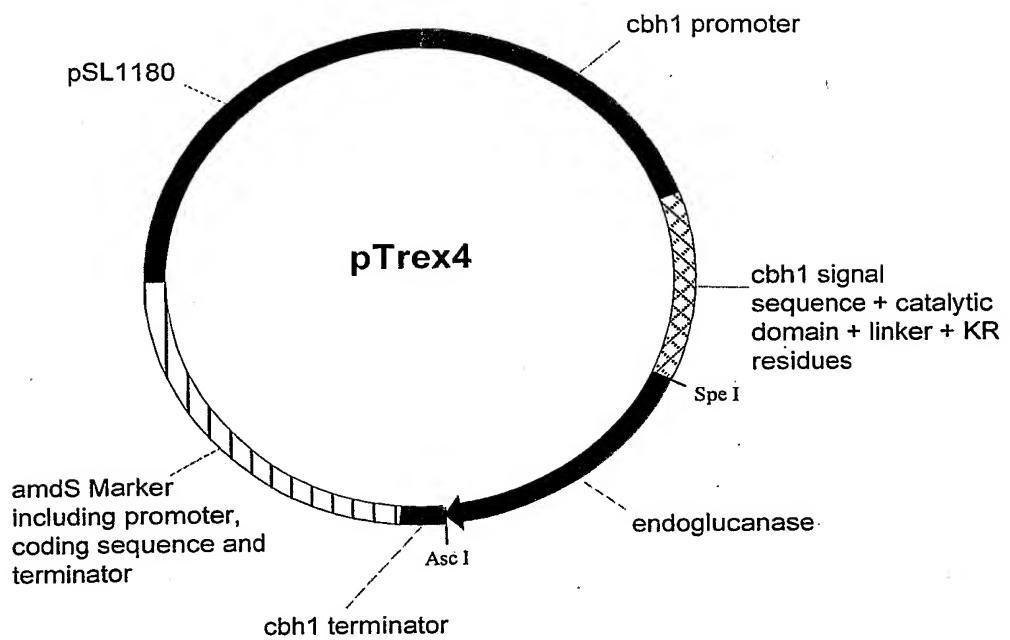


Figure 17

DNA sequence of pTrex4 (10239 bases)

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ACCCCCAACCTCCATTACGCCCTCCCCATAGAGTTCCAATCAGTGAGTCATG
GCACTGTTCTCAAATAGATTGGGGAGAAGTTGACTTCCGCCAGAGCTGAAG
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CACCGAAAAGCAAGATGTTGCGATCTAACATCCAGGAACCTGGATACATCC
ATCATCACGCACGACCACTTGATCTGCTGGTAAACTCGTATTGCCCTAAAC
CGAAGTGACGTGGTAAATCTACACGTGGGCCCTTCGGTATACTGCGTGTGT
CTTCTCTAGGTGCCATTCTTCCCTCCTAGTGTGAATTGTTGTGTGG
AGTCCGAGCTGTAACACCTCTGAATCTCTGGAGAATGGTGGACTAACGACT
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TGCTCTTGAGCTACAAGAACCTGTGGGTATATATCTAGAGTTGTGAAGTC
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GCGAACCCGGAGAATCGAGATGTGCTGGAAAGCTCTAGCGAGCGGCTAAAT
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TACCGTACAAGTCGTAATCACTATTAACCCAGACTGACCGGACGTGTTG
CCTTCATTGGAGAAATAATGTCATTGCGATGTGTAATTGCCCTGCTTGACCG
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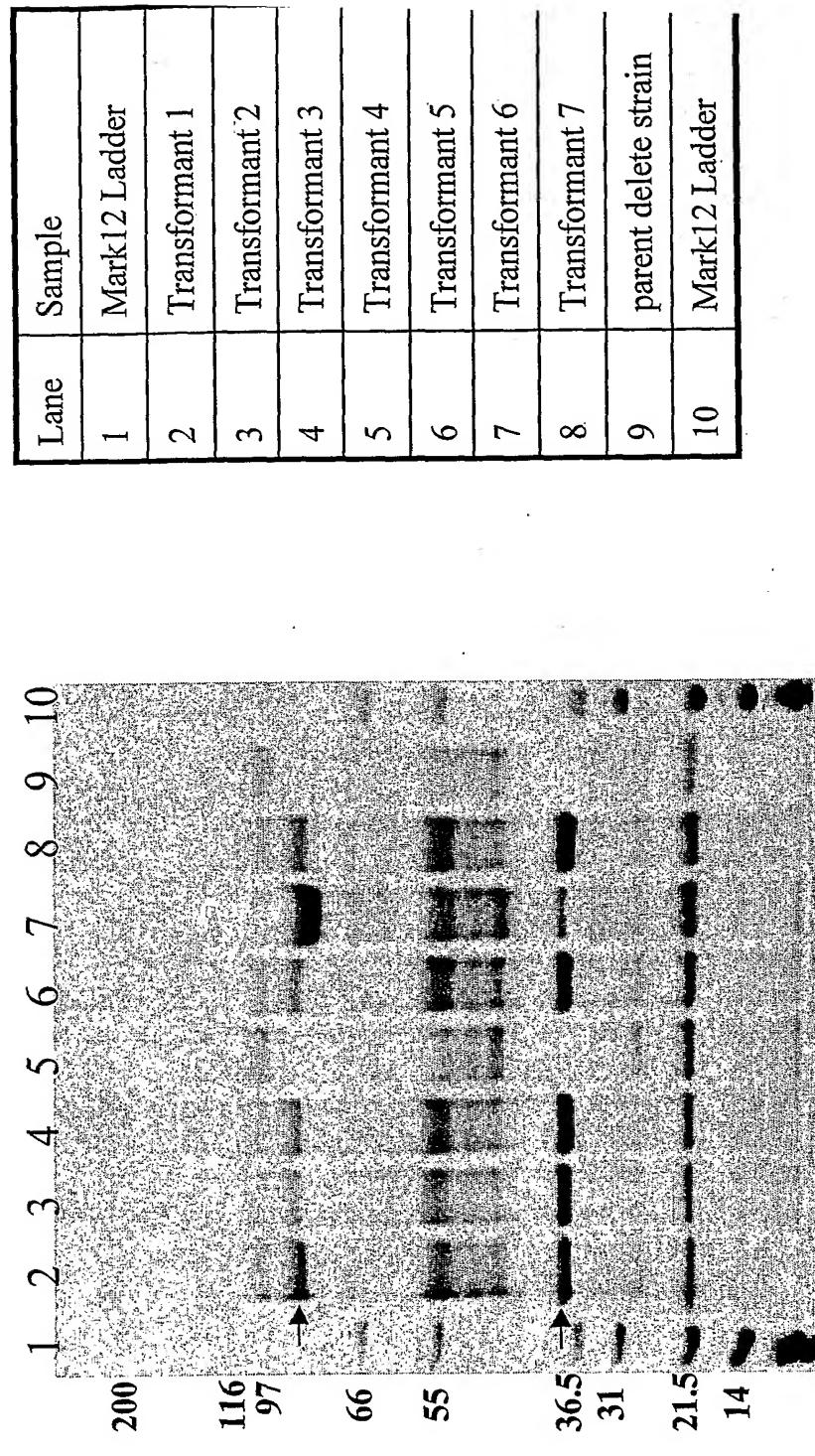
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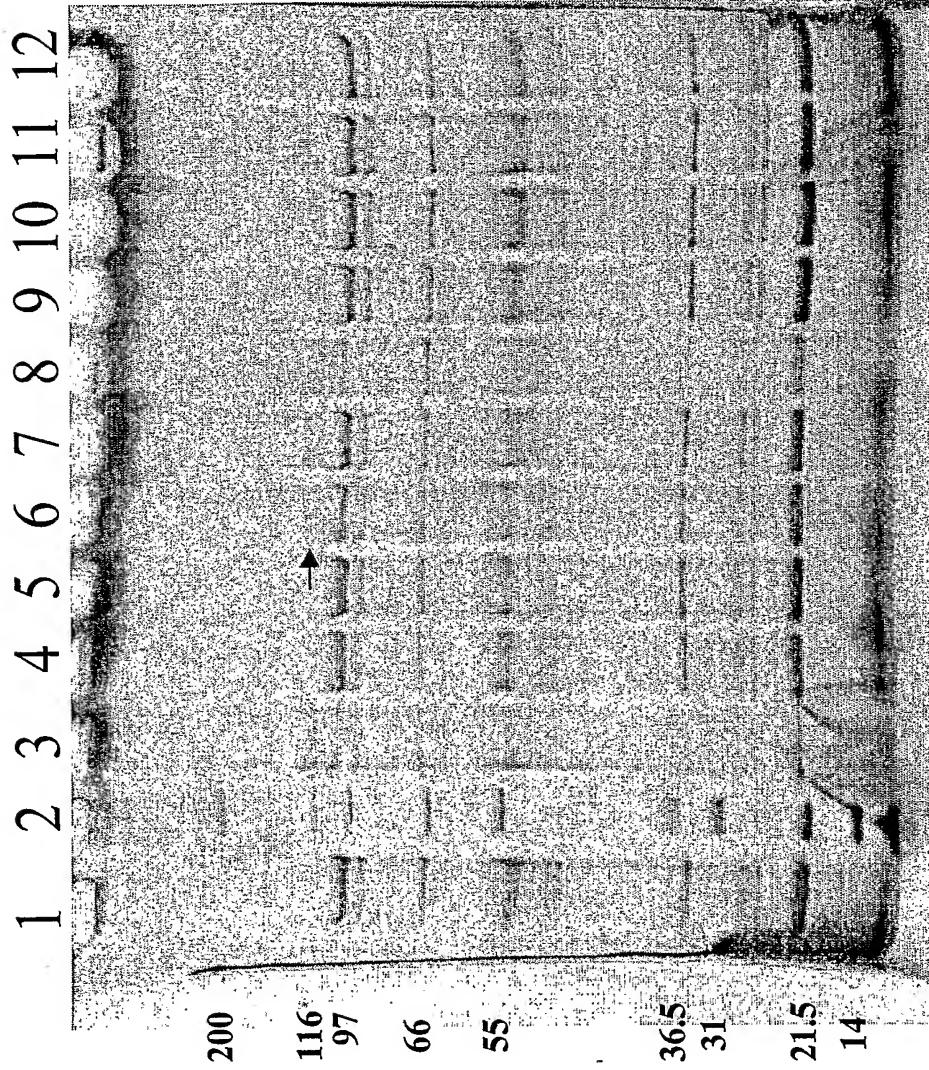
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Figure 18
SDS-PAGE gel of supernate samples of shake flask grown *T. reesei* delete strain transformed with the fusion expression construct *cbhl-E1*



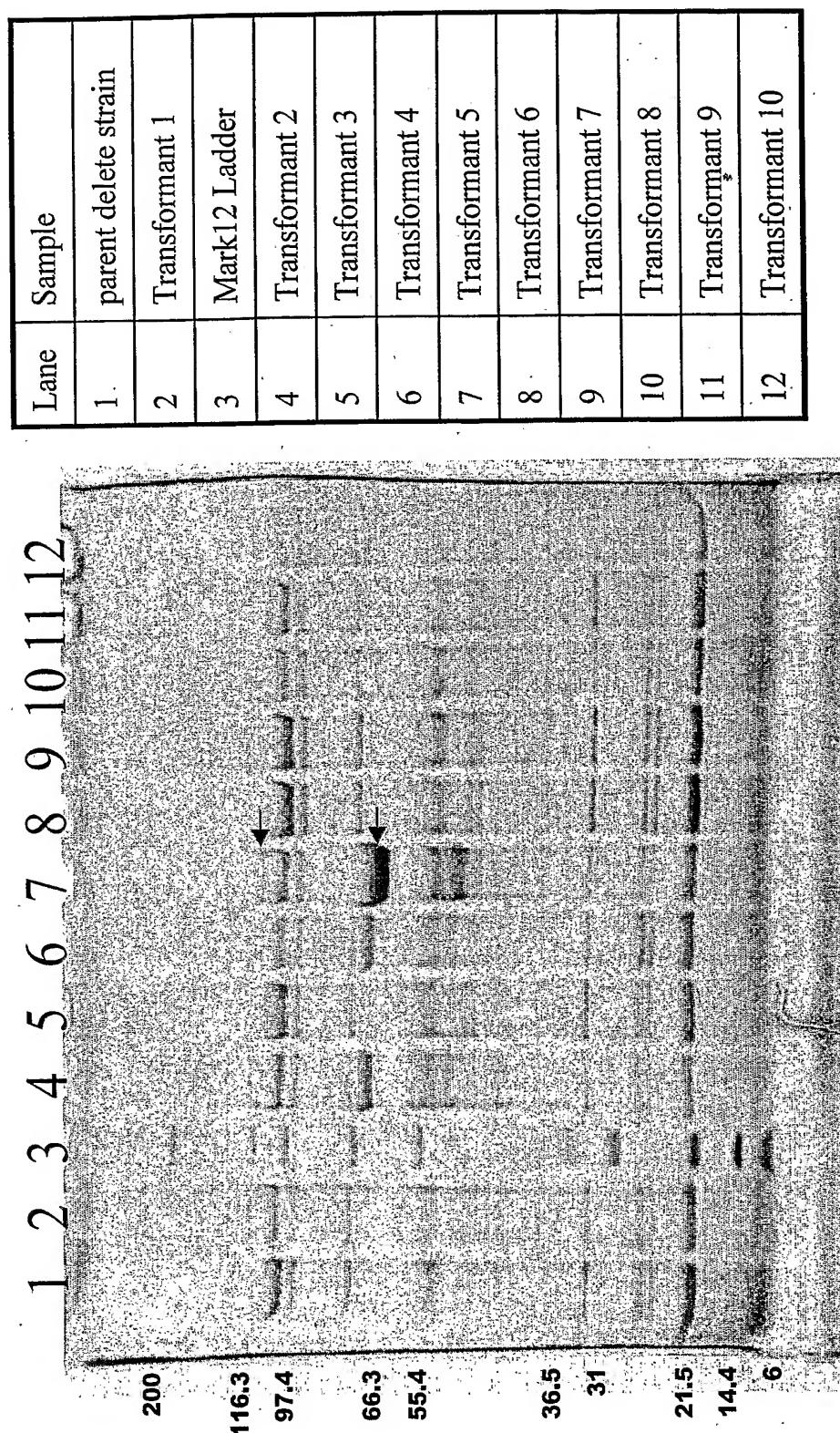
The fusion protein is indicated by the upper arrow, the cleaved E1 catalytic domain is indicated by the lower arrow

Figure 19
SDS-PAGE gel of supernate samples of shake flask grown *T. reesei* delete strain
transformed with the fusion expression construct *cbb1-GH48*



The fusion protein is indicated by the arrow

Figure 20
 SDS-PAGE gel of supernate samples of shake grown *T. reesei* delete strain
 transformed with the fusion expression construct *cbl1-GH74*



The fusion protein is indicated by the upper arrow, the cleaved GH74 catalytic domain is indicated by the lower arrow.

Figure 21
 SDS-PAGE gel of supernate samples of shake flask grown *T. reesei* delete strain transformed with the fusion expression construct *cbh1-E3*

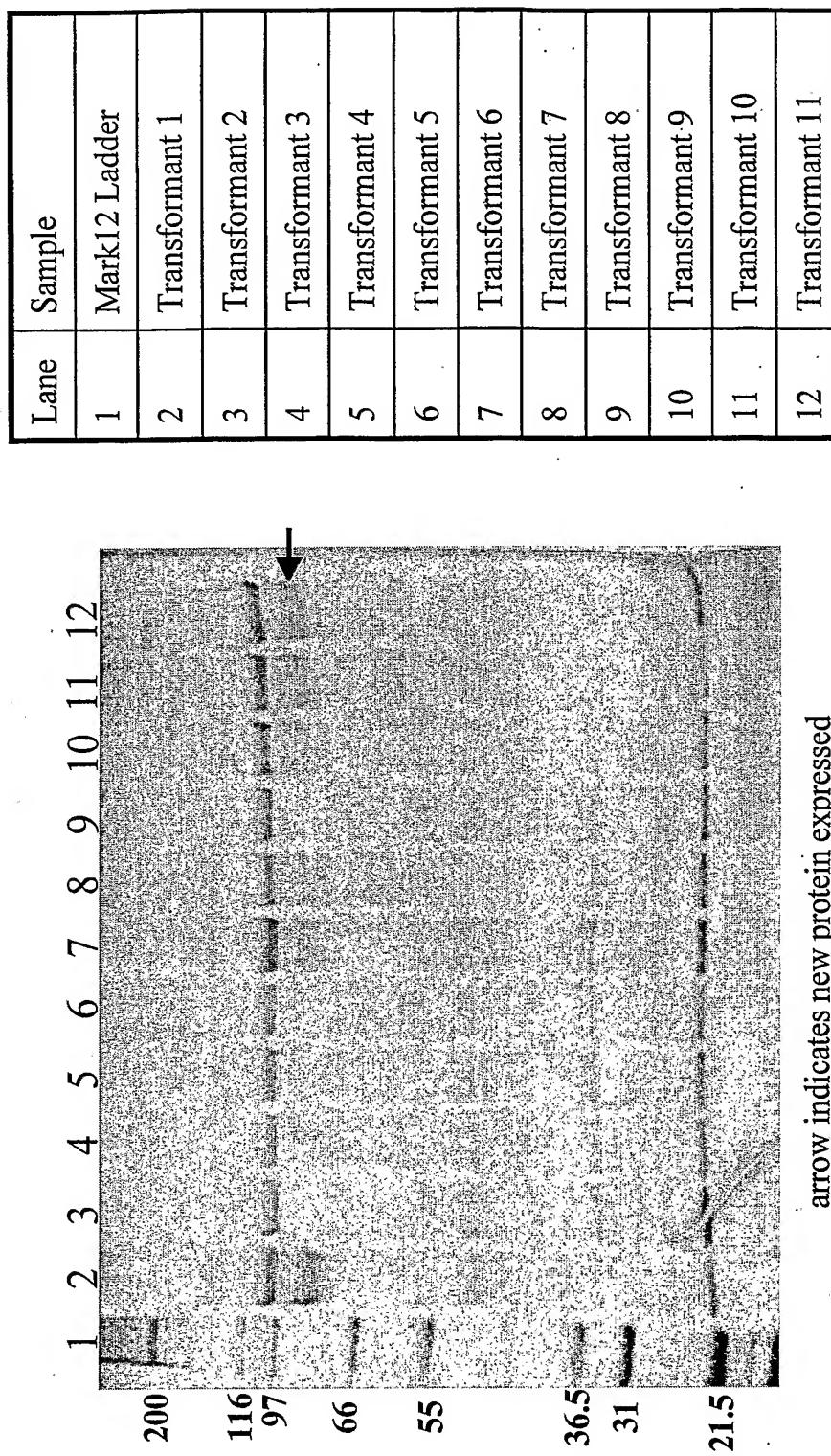


Figure 22
 SDS-PAGE gel of supernate samples of shake flask grown *T. reesei* delete strain
 transformed with the fusion expression construct cbh1-E5

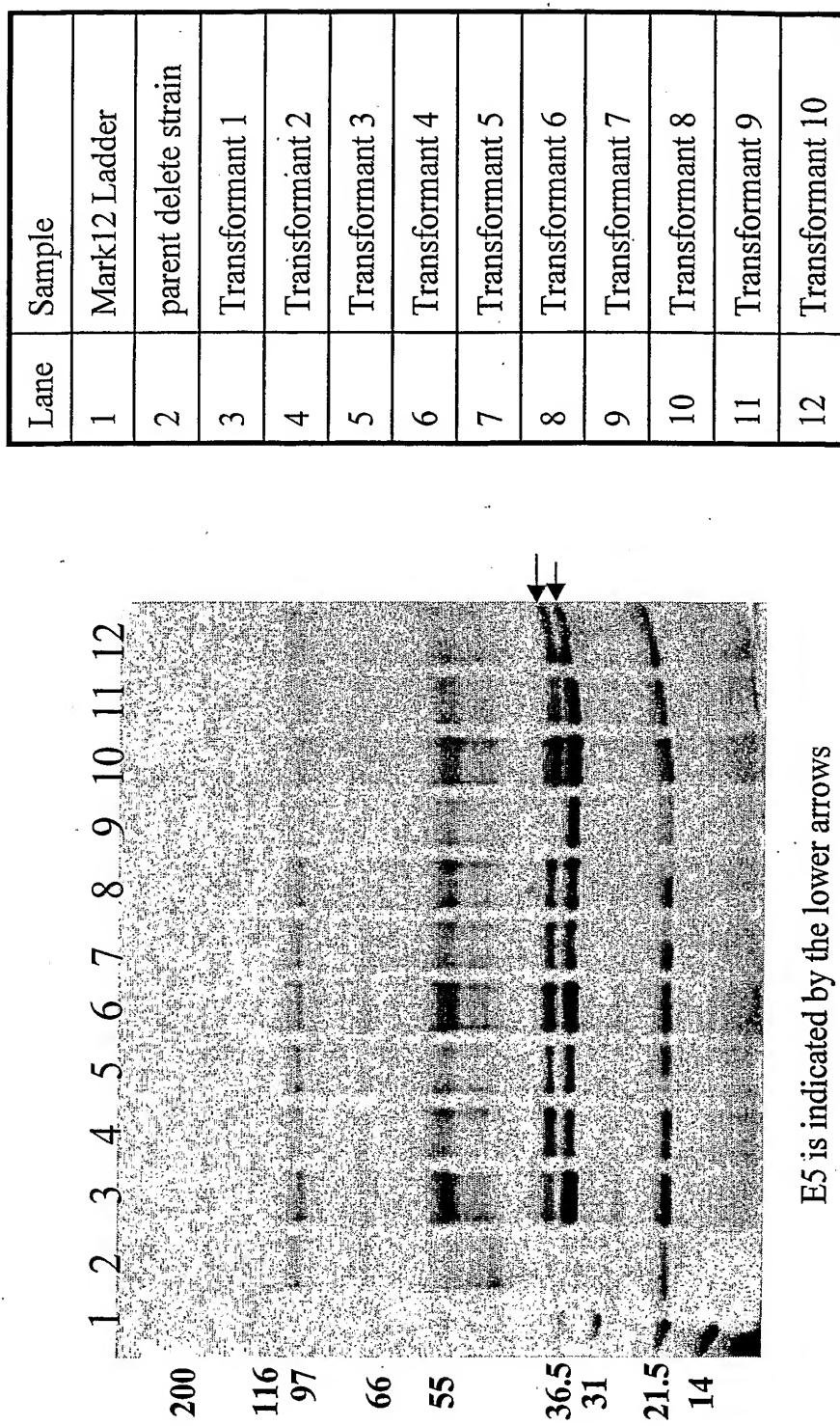


FIGURE 23

